

Protein: SEQUENCE COMPARISON w/ WO/0018915

ID AAY84609 standard; protein; 230 AA.
 DT 25-JUL-2000 (first entry)
 XX
 DE A human membrane associated organizational protein (HJNCT).
 XX
 KW Human; membrane associated organizational protein; HJNCT;
 KW cell proliferative disorder; cancer; autoimmune disorder;
 KW inflammatory disorder; neurological disorder; developmental disorder;
 KW vesicle trafficking; reproductive disorder; gastrointestinal disorder;
 KW renal disorder; atherosclerosis; leukaemia; rheumatoid arthritis;
 KW Alzheimer's disease; anxiety; diabetes; ovulatory defect; renal failure;
 KW irritable bowel syndrome; allergy.

OS Homo sapiens.

XX
 FH Key Location/Qualifiers
 FT Modified-site 29
 FT /note= "potential phosphorylation site"
 FT Modified-site 62
 FT /note= "potential phosphorylation site"
 FT Domain 117..138
 FT /note= "transmembrane domain"
 FT Modified-site 155
 FT /note= "potential phosphorylation site"
 FT Domain 164..182
 FT /note= "transmembrane domain"
 FT Modified-site 187
 FT /note= "potential phosphorylation site"
 FT Modified-site 190
 FT /note= "potential glycosylation site"
 FT Modified-site 208
 FT /note= "potential phosphorylation site"
 FT Modified-site 224
 FT /note= "potential phosphorylation site"

PN WO200018915-A2.

PD 06-APR-2000.

PF 23-SEP-1999; 99WO-US022082.

PR 25-SEP-1998; 98US-0155215P.

PR 13-OCT-1998; 98US-0155251P.

PR 04-MAY-1999; 99US-0172228P.

PA (INCY-) INCYTE PHARM INC.

PI Yue H, Lal P, Corley NC, Guegler KJ, Baughn MR, Lu AD, Tang YT;

DR WPI; 2000-293154/25.

DR N-PSDB; AAA12585.

PT Human membrane associated organizational protein and nucleic acid
 PT sequences useful in the diagnosis, treatment and prevention of cell
 PT proliferative associated disorders e.g. cancer, rheumatoid arthritis and
 PT Alzheimer's disease.

XX

PS Claim 1; Page 76-77; 84pp; English.

XX

The present sequence represents a membrane associated organizational protein (HJNCT). HJNCT is used for the diagnosis, treatment and prevention of cell proliferative disorders including cancer and autoimmune/inflammatory, neurological, developmental, vesicle trafficking, reproductive, gastrointestinal and renal disorders. These disorders may include atherosclerosis, leukaemia, allergies, rheumatoid arthritis, Alzheimer's disease, anxiety, diabetes, ovulatory defects, renal failure and irritable bowel syndrome. A vector expressing HJNCT, and an agonist of HJNCT can be used to treat or prevent a disorder associated with decreased expression or activity of HJNCT. An antagonist of HJNCT or a vector expressing the complement of a polynucleotide encoding HJNCT can be used to treat or prevent a disorder associated with increased expression or activity of HJNCT. Antibodies which bind HJNCT can be used for diagnosis of disorders associated with HJNCT expression or to monitor patients being treated with HJNCT, agonists, antagonists or inhibitors of HJNCT. Assays are preferably carried out on body fluids from a patient using radioimmunoassay, enzyme linked immunosorbent assays or fluorescent activated cell sorting assays. Polynucleotides encoding HJNCT are also used in hybridisation assays to determine absence, presence or excess expression of HJNCT and to monitor regulation of HJNCT levels during disease therapy

XX

SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 3; Length 230;
Best Local Similarity 100.0%; Pred. No. 7.3e-117;
Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

NUCLEIC ACID: SEQUENCE COMPARISONS w/ WP/0018915

AF177340 1839 GGACAGGAAGGCAGCCTGGGACATTTAAAAAAA

→ >10 P_AAA12585 cDNA encoding a membrane associated organizational protein (HJNCT). (2742 bp) [1 seg]

Score = 1472 (2918 bits), Expect = 0.0

Identities = 1472/1472 (100%), at 4,1-1475,1472, Strand +/-

ss.DNA64886 4 AGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA

P_AAA12585 1 AGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCAAGA

ss.DNA64886 64 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCAT

P_AAA12585 61 GCTTCAGCCTGAAGACAAGGGAGCAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCAT

ss.DNA64886 124 GGCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCAC

P_AAA12585 121 GGCCTCTCTTGGCCTCCAACCTGTGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCAC

ss.DNA64886 184 ACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGT

P_AAA12585 181 ACTGGTTGCCATGCTGCTCCCCAGCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGT

ss.DNA64886 244 GACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCAT

P_AAA12585 241 GACAGCAGTTGGCTTCTCCAAGGGCCTCTGGATGGAATGTGCCACACACAGCACAGGCAT

ss.DNA64886 304 CACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCCA

P_AAA12585 301 CACCCAGTGTGACATCTATAGCACCTTCTGGGCCTGCCCGCTGACATCCAGGCTGCCCCA

ss.DNA64886 364 GGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGG

P_AAA12585 361 GGCCATGATGGTGACATCCAGTGCAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGG

ss.DNA64886 424 CATGAGATGCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG

P_AAA12585 421 CATGAGATGCACAGTCTTCTGCCAGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGG

ss.DNA64886 484 TGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCA

P_AAA12585 481 TGGAGTCTTTTTCATCCTTGGAGGCCTCCTGGGATTCATTCCTGTTGCCTGGAATCTTCA

ss.DNA64886 544 TGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGG

P_AAA12585 541 TGGGATCCTACGGGACTTCTACTCACCCTGGTGCCTGACAGCATGAAATTTGAGATTGG

ss.DNA64886 604 AGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCT

P_AAA12585 601 AGAGGCTCTTTACTTGGGCATTATTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCT

ss.DNA64886 664 CTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCA

P_AAA12585 661 CTGCTTTTCTGCTCATCCAGAGAAATCGCTCCAACCTACTACGATGCCTACCAAGCCCA

ss.DNA64886 724 ACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTT

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*****
P_AAA12585 721 ACCTCTTGCCACAAGGAGCTCTCCAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTT
ss.DNA64886 784 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGC
*****
P_AAA12585 781 CAATTCCTACAGCCTGACAGGGTATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGC
ss.DNA64886 844 TGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT
*****
P_AAA12585 841 TGGGTCTGTGAAAAACAGTGGACAGCACCCCGAGGGCCACAGGTGAGGGACACTACCACT
ss.DNA64886 904 GGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAG
*****
P_AAA12585 901 GGATCGTGTGAGAAGGTGCTGCTGAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAG
ss.DNA64886 964 GCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGC
*****
P_AAA12585 961 GCAGAAATGGGGGCTAGTGTAACAGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGC
ss.DNA64886 1024 CAGCCTTTCTGTTTTCTCCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACT
*****
P_AAA12585 1021 CAGCCTTTCTGTTTTCTCCTCACCTTGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACT
ss.DNA64886 1084 GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGG
*****
P_AAA12585 1081 GAAACCCCATTCCTTAAGCCAGGACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGG
ss.DNA64886 1144 ACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGACCC
*****
P_AAA12585 1141 ACTCCATCCCCAAACCCACTAATCACATCCCCTGACTGACCCTCTGTGATCAAAGACCC
ss.DNA64886 1204 TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGC
*****
P_AAA12585 1201 TCTCTCTGGCTGAGGTTGGCTCTTAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGC
ss.DNA64886 1264 TTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
*****
P_AAA12585 1261 TTTTGTGGGCATTGCTCTAACCTACTTCTCAAGCTTCCCTCCAAAGAACTGATTGGCCC
ss.DNA64886 1324 TGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAA
*****
P_AAA12585 1321 TGGAACCTCCATCCCCTCTTGTTATGACTCCACAGTGTCCAGACTAATTTGTGCATGAA
ss.DNA64886 1384 CTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGA
*****
P_AAA12585 1381 CTGAAATAAAACCATCCTACGGTATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGA
ss.DNA64886 1444 CAGGAAGGCAGCCTGGGACATTTAAAAAATA
*****
P_AAA12585 1441 CAGGAAGGCAGCCTGGGACATTTAAAAAATA

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>11 P_AAF93769 Human cDNA encoding a membrane or secretory protein clone
PSEC0059. (2863 bp) [1 seg]

Score = 1464 (2902 bits), Expect = 0.0

Identities = 1470/1472 (99%), at 1,110-1472,1581, Strand +/+

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ss.DNA64886 1 GAGAGAAGTCAGCCTGGCAGAGAGACTCTGAAATGAGGGATTAGAGGTGTTCAAGGAGCA

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Protein: SEQUENCE COMPARISON w/ W09925825

ID AAY36181 standard; protein; 230 AA.
 DT 23-SEP-1999 (first entry)
 XX
 DE Human secreted protein #53.
 KW Secreted protein; human; cytostatic; thrombotic; osteopathic; forensic;
 KW diagnostic; gene therapy; chromosome mapping; secretion vector.
 PN W09925825-A2.
 PD 27-MAY-1999.
 PF 13-NOV-1998; 98WO-IB001862.
 XX
 PR 13-NOV-1997; 97US-0066677P.
 PR 17-DEC-1997; 97US-0069957P.
 PR 09-FEB-1998; 98US-0074121P.
 PR 13-APR-1998; 98US-0081563P.
 PR 10-AUG-1998; 98US-0096116P.
 PR 04-SEP-1998; 98US-0099273P.
 XX
 PA (GEST) GENSET.
 XX
 PI Bougueleret L, Duclert A, Dumas Milne Edwards J;
 XX
 DR WPI; 1999-347472/29.
 DR N-PSDB; AAX97865.
 XX
 PT Extended cDNAs encoding secreted proteins.
 XX
 PS Claim 7; Page 289; 307pp; English.
 XX
 CC AAY36129-Y36222 represent novel human secreted proteins encoded by the
 CC extended cDNA sequences represented in AAX97813-X97906. The proteins of
 CC the invention have cytostatic, thrombotic and osteopathic activity. The
 CC extended cDNAs can be used to express secreted proteins or parts of them
 CC or to obtain antibodies capable of binding to the secreted proteins. They
 CC may also be used in diagnostic, forensic, gene therapy and chromosome
 CC mapping procedures. Uses also include design of expression vectors and
 CC secretion vectors
 XX
 SQ Sequence 230 AA;

Query Match 100.0%; Score 1174; DB 2; Length 230;
 Best Local Similarity 100.0%; Pred. No. 7.3e-117;
 Matches 230; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MASLGLQLVGYYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTG	60
Db	1	MASLGLQLVGYYILGLLGLLGLTLVAMLLPSWKTSSYVGASIVTAVGFSKGLWMECATHSTG	60
Qy	61	ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVA	120
Db	61	ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIIISVVGMRCTVFCQESRAKDRVAVA	120
Qy	121	GGVFFILGGLLGFIPVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGII	180
Db	121	GGVFFILGGLLGFIPVAVNLHGILRDFYSPLVPDSMKFEIGEALYLGIISSLFSLIAGII	180
Qy	181	LCFSCSSQRNRSNYYDAYQAQPLATRSSPRPGQPPKVKSEFNLSYSLTGYY	230

Db

181 LCFSCSSQRNRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSYSLTGYV 230

Nucleic Acid: SEQUENCE COMPARISON w/w0/9925825

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ss.DNA64886 887 TGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGC
*****
AX286822 842 TGAGGGACACTACCACTGGATCGTGTCAGAAGGTGCTGCTGAGGATAGACTGACTTTGGC
ss.DNA64886 947 CATTGGA TTGAGCAAAGGAGGAT-GGGGCTAGTGTAACAGCATGCAGGTGAATTG
*****
AX286822 902 CATTGGATTGAGCAAAGGAGGAT-GGGGCTAGTGTAACAGCATGCAGGTGAATTG
ss.DNA64886 1005 CCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTCCCTGCCCTA
*****
AX286822 962 CCAAGGATGCTCGCCATGCCAGCCTTCTGTTTTCTCACCTTGCTGCTCCCTGCCCTA
ss.DNA64886 1065 AGTCCCAACCCCTCACTTGAACCCCAATTCCTTAAGCCAGGACTCAGAGGATCCCTTT
*****
AX286822 1022 AGTCCCAACCCCTCACTTGAACCCCAATTCCTTAAGCCAGGACTCAGAGGATCCCTTT
ss.DNA64886 1125 GCTCTGCTTTAATCTGGGACTCCATCCCAACCCCACTAATCAATCCCACTGACTGAC
*****
AX286822 1082 GCTCTGCTTTAATCTGGGACTCCATCCCAACCCCACTAATCAATCCCACTGACTGAC
ss.DNA64886 1185 CCTCTGTGATCAAGACCCTCTCTGCTGAGGTGGCTCTTAGCTCATTGCTGGGGAT
*****
AX286822 1142 CCTCTGTGATCAAGACCCTCTCTGCTGAGGTGGCTCTTAGCTCATTGCTGGGGAT
ss.DNA64886 1245 GGGAGGAGAGCAGTGGCTTTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCTC
*****
AX286822 1202 GGGAGGAGAGCAGTGGCTTTTGTGGCATTGCTCTAACCTACTTCTCAAGCTTCCTC
ss.DNA64886 1305 CAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTC
*****
AX286822 1262 CAAGAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGTATGACTCCACAGTGTC
ss.DNA64886 1365 AGACTAATTGTGTCATGAAGTAAATAAATCATCTACGCTATCCAGGAACAGAAAGC
*****
AX286822 1322 AGACTAATTGTGTCATGAAGTAAATAAATCATCTACGCTATCCAGGAACAGAAAGC
ss.DNA64886 1425 AGGATGCAAGTGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA
*****
AX286822 1382 AGGATGCAAGTGGGAGGACAGGAAGGCAGCCTGGGACATTTAAAAAATA

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>18 P_AAX97865 Human secreted protein encoding cDNA #53. cDNA, PAT 23-SEP-1999 (1400 bp) [1 seg]

Score = 1381 (2738 bits), Expect = 0.0

Identities = 1387/1389 (99%), at 87,1-1475,1389, Strand +/-

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ss.DNA64886 87 CAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTCTTGGCCTCCAATTG
*****
P_AAX97865 1 CAGTCCCTGAAGACGCTTCTACTGAGAGGTCTGCCATGGCCTCTCTTGGCCTCCAATTG
ss.DNA64886 147 TGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCATGCTGCTCCCCA
*****
P_AAX97865 61 TGGGCTACATCCTAGGCCTTCTGGGGCTTTTGGGCACACTGGTTGCCATGCTGCTCCCCA
ss.DNA64886 207 GCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAGCAGTTGGCTTCTCCAAGG
*****
P_AAX97865 121 GCTGGAAAACAAGTTCTTATGTGGTGCCAGCATTGTGACAGCAGTTGGCTTCTCCAAGG

```

ss.DNA64886 267 GCCTCTGGATGGAATGTGCCACACAGCACAGGCATCACCCAGTGTGACATCTATAGCA

P_AAX97865 181 GCCTCTGGATGGAATGTGCCACACAGCACAGGCATCACCCAGTGTGACATCTATAGCA

ss.DNA64886 327 CCCTTCTGGGCCTGCCCGTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTG

P_AAX97865 241 CCCTTCTGGGCCTGCCCGTGACATCCAGGCTGCCCAGGCCATGATGGTGACATCCAGTG

ss.DNA64886 387 CAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCC

P_AAX97865 301 CAATCTCCTCCCTGGCCTGCATTATCTCTGTGGTGGGCATGAGATGCACAGTCTTCTGCC

ss.DNA64886 447 AGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAG

P_AAX97865 361 AGGAATCCCGAGCCAAAGACAGAGTGGCGGTAGCAGGTGGAGTCTTTTTTCATCCTTGGAG

ss.DNA64886 507 GCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACT

P_AAX97865 421 GCCTCCTGGGATTCAATCCTGTTGCCTGGAATCTTCATGGGATCCTACGGGACTTCTACT

ss.DNA64886 567 CACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTA

P_AAX97865 481 CACCACTGGTGCCTGACAGCATGAAATTTGAGATTGGAGAGGCTCTTTACTTGGGCATTA

ss.DNA64886 627 TTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGA

P_AAX97865 541 TTTCTTCCCTGTTCTCCCTGATAGCTGGAATCATCCTCTGCTTTTCTGCTCATCCCAGA

ss.DNA64886 687 GAAATCGCTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTC

P_AAX97865 601 GAAATCGCTCCAATACTACGATGCCTACCAAGCCCAACCTCTTGCCACAAGGAGCTCTC

ss.DNA64886 747 CAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT

P_AAX97865 661 CAAGGCCTGGTCAACCTCCCAAAGTCAAGAGTGAGTTCAATTCCTACAGCCTGACAGGGT

ss.DNA64886 807 ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGAC

P_AAX97865 721 ATGTGTGAAGAACCAGGGGCCAGAGCTGGGGGGTGGCTGGGTCTGTGAAAAACAGTGGAC

ss.DNA64886 867 AGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCT

P_AAX97865 781 AGCACCCCGAGGGCCACAGGTGAGGGACACTACCACTGGATCGTGTGAGAAGGTGCTGCT

ss.DNA64886 927 GAGGATAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAC
**** *****
P_AAX97865 841 GAGGGTAGACTGACTTTGGCCATTGGATTGAGCAAAGGCAGAAATGGGGGCTAGTGTAAC
↑

ss.DNA64886 987 AGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCCTCACCT

P_AAX97865 901 AGCATGCAGGTTGAATTGCCAAGGATGCTCGCCATGCCAGCCTTTCTGTTTTCCTCACCT

ss.DNA64886 1047 TGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTTAAGCCAG

P_AAX97865 961 TGCTGCTCCCCTGCCCTAAGTCCCCAACCCCTCAACTTGAAACCCCATTCCTTTAAGCCAG

ss.DNA64886 1107 GACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAAT

 P_AAX97865 1021 GACTCAGAGGATCCCTTTGCCCTCTGGTTTACCTGGGACTCCATCCCCAAACCCACTAAT

 ss.DNA64886 1167 CACATCCCACTGACTGACCCTCTGTGATCAAAGACCCTCTCTCTGGCTGAGGTTGGCTCT

 P_AAX97865 1081 CACATCCCACTGACTGACCCTCTGTGATCAAAGACCCTCCCTCTGGCTGAGGTTGGCTCT
 4
 ss.DNA64886 1227 TAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCT

 P_AAX97865 1141 TAGCTCATTGCTGGGGATGGGAAGGAGAAGCAGTGGCTTTTGTGGGCATTGCTCTAACCT

 ss.DNA64886 1287 ACTTCTCAAGCTTCCCTCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGT

 P_AAX97865 1201 ACTTCTCAAGCTTCCCTCCAAAGAAACTGATTGGCCCTGGAACCTCCATCCCACTCTTGT

 ss.DNA64886 1347 TATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGT

 P_AAX97865 1261 TATGACTCCACAGTGTCCAGACTAATTTGTGCATGAACTGAAATAAAACCATCCTACGGT

 ss.DNA64886 1407 ATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTT

 P_AAX97865 1321 ATCCAGGGAACAGAAAGCAGGATGCAGGATGGGAGGACAGGAAGGCAGCCTGGGACATTT

 ss.DNA64886 1467 AAAAAAATA

 P_AAX97865 1381 AAAAAAATA

Query Match 93.4%; Score 1096; DB 1; Length 230;
Best Local Similarity 91.3%; Pred. No. 1.4e-85;
Matches 210; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

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Qy      1 MASLGLQLVGYYILGLLGLLGLTLVAMLLPSWKTSYVVGASIVTAVGFSKGLWMECATHSTG 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MASLGVQLVGYYILGLLGLLGLTGIAMLLPNWRTSSYVVGASIVTAVGFSKGLWMECATHSTG 60

Qy     61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAIISSLACIISVVGMRCTVFCQESRAKDRVAVA 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 61 ITQCDIYSTLLGLPADIQAAQAMMVTSSAMSSLACII SVVGMRCTVFCQDSRAKDRVAVV 120

Qy 121 GGVFFILGGLLGFI PVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGII SSLFSLIAGII 180
| | | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | : | | | | : | | :

Db 121 GGVFFILGGILGFI PVAWNLHGILRDFYSPLVPDSMKFEIGEALYLGII SALFSLVAGVI 180

Qy 181 LCFSCSSQRNRSNYDAYQAQPLATRSSPRPGQPPKVKSEFNSSYSLTGYV 230
| | | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | |

Db 181 LCFSCSPQGNRTNYDGYQAQPLATRSSPRSAQQPKAKSEFNSSYSLTGYV 230